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301

TCAAGGACGGTGACTGGAATGAATTCCGTCGTAAACTGACCTTCTATCTGAAAACCTTGG

-----+-----+-----+-----+-----+-----+ 360

AGTTCCTGCCACTGACCTTACTTAAGGCAGCATTTGACTGGAAGATAGACTTTTGGAACC

LysAspGlyAspTrpAsnGluPheArgArgLysLeuThrPheTyrLeuLysThrLeuGlu

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361

AGAACGCGCAGGCTCAACAGACCACTCTGTCGCTAGCGATCTTTTAATAAGCTT [SEQ ID NO: 147]

-----+-----+-----+-----+-----+-----+ 414

TCTTGCGCGTCCGAGTTGTCTGGTGAGACAGCGATCGCTAGAAAATTATTCGAA [SEQ ID NO: 148]

AsnAlaGlnAlaGlnGlnThrThrLeuSerLeuAlaIlePheEndEnd [SEQ ID NO: 128]

F i g -

3B